

Serial Number:

09/869,334

CRF Processing Date

10/4/2001

Edited by

Verified by

(STIC stat

**ENTERED**☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_☐

Added the mandatory heading and subheadings for "Current Application Data"

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings-used by an applicant, specifically:

☐Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_☐

Inserted mandatory headings, specifically: \_\_\_\_\_

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

☒

Other:

Deleted extra headings

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form

3/1/95

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,334

DATE: 10/04/2001

TIME: 12:48:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 6 <120> TITLE OF INVENTION: A Process for producing HMG-CoA Reductase inhibitor  
 8 <130> FILE REFERENCE: H11-0011T4  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/869,334  
 C--> 10 <141> CURRENT FILING DATE: 2001-07-14  
 10 <160> NUMBER OF SEQ ID NOS: 45  
 12 <170> SOFTWARE: PatentIn Ver. 2.0  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 396  
 16 <212> TYPE: PRT  
 17 <213> ORGANISM: Bacillus subtilis  
 19 <400> SEQUENCE: 1  
 20 Met Asn Val Leu Asn Arg Arg Gln Ala Leu Gln Arg Ala Leu Leu Asn  
 21 1 5 10 15  
 23 Gly Lys Asn Lys Gln Asp Ala Tyr His Pro Phe Pro Trp Tyr Glu Ser  
 24 20 25 30  
 26 Met Arg Lys Asp Ala Pro Val Ser Phe Asp Glu Glu Asn Gln Val Trp  
 27 35 40 45  
 29 Ser Val Phe Leu Tyr Asp Asp Val Lys Lys Val Val Gly Asp Lys Glu  
 30 50 55 60  
 32 Leu Phe Ser Ser Cys Met Pro Gln Gln Thr Ser Ser Ile Gly Asn Ser  
 33 65 70 75 80  
 35 Ile Ile Asn Met Asp Pro Pro Lys His Thr Lys Ile Arg Ser Val Val  
 36 85 90 95  
 38 Asn Lys Ala Phe Thr Pro Arg Val Met Lys Gln Trp Glu Pro Arg Ile  
 39 100 105 110  
 41 Gln Glu Ile Thr Asp Glu Leu Ile Gln Lys Phe Gln Gly Arg Ser Glu  
 42 115 120 125  
 44 Phe Asp Leu Val His Asp Phe Ser Tyr Pro Leu Pro Val Ile Val Ile  
 45 130 135 140  
 47 Ser Glu Leu Leu Gly Val Pro Ser Ala His Met Glu Gln Phe Lys Ala  
 48 145 150 155 160  
 50 Trp Ser Asp Leu Leu Val Ser Thr Pro Lys Asp Lys Ser Glu Glu Ala  
 51 165 170 175  
 53 Glu Lys Ala Phe Leu Glu Glu Arg Asp Lys Cys Glu Glu Glu Leu Ala  
 54 180 185 190  
 56 Ala Phe Phe Ala Gly Ile Ile Glu Glu Lys Arg Asn Lys Pro Glu Gln  
 57 195 200 205  
 59 Asp Ile Ile Ser Ile Leu Val Glu Ala Glu Glu Thr Gly Glu Lys Leu  
 60 210 215 220  
 62 Ser Gly Glu Glu Leu Ile Pro Phe Cys Thr Leu Leu Leu Val Ala Gly  
 63 225 230 235 240  
 65 Asn Glu Thr Thr Thr Asn Leu Ile Ser Asn Ala Met Tyr Ser Ile Leu  
 66 245 250 255  
 68 Glu Thr Pro Gly Val Tyr Glu Glu Leu Arg Ser His Pro Glu Leu Met  
 69 260 265 270  
 71 Pro Gln Ala Val Glu Glu Ala Leu Arg Phe Arg Ala Pro Ala Pro Val

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```

72          275          280          285
74 Leu Arg Arg Ile Ala Lys Arg Asp Thr Glu Ile Gly Gly His Leu Ile
75          290          295          300
77 Lys Glu Gly Asp Met Val Leu Ala Phe Val Ala Ser Ala Asn Arg Asp
78 305          310          315          320
80 Glu Ala Lys Phe Asp Arg Pro His Met Phe Asp Ile Arg Arg His Pro
81          325          330          335
83 Asn Pro His Ile Ala Phe Gly His Gly Ile His Phe Cys Leu Gly Ala
84          340          345          350
86 Pro Leu Ala Arg Leu Glu Ala Asn Ile Ala Leu Thr Ser Leu Ile Ser
87          355          360          365
89 Ala Phe Pro His Met Glu Cys Val Ser Ile Thr Pro Ile Glu Asn Ser
90          370          375          380
92 Val Ile Tyr Gly Leu Lys Ser Phe Arg Val Lys Met
93 385          390          395
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 1191
98 <212> TYPE: DNA
99 <213> ORGANISM: Bacillus subtilis
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)..(1191)
105 <400> SEQUENCE: 2
106 atg aat gtg tta aac cgc cgg caa gcc ttg cag cga gcg ctg ctc aat 48
107 Met Asn Val Leu Asn Arg Arg Gln Ala Leu Gln Arg Ala Leu Leu Asn
108 1 5 10 15
110 ggg aaa aac aaa cag gat gcg tat cat ccg ttt cca tgg tat gaa tcg 96
111 Gly Lys Asn Lys Gln Asp Ala Tyr His Pro Phe Pro Trp Tyr Glu Ser
112 20 25 30
114 atg aga aag gat gcg cct gtt tcc ttt gat gaa gaa aac caa gtg tgg 144
115 Met Arg Lys Asp Ala Pro Val Ser Phe Asp Glu Glu Asn Gln Val Trp
116 35 40 45
118 agc gtt ttt ctt tat gat gat gtc aaa aaa gtt gtt ggg gat aaa gag 192
119 Ser Val Phe Leu Tyr Asp Asp Val Lys Lys Val Val Gly Asp Lys Glu
120 50 55 60
122 ttg ttt tcc agt tgc atg ccg cag cag aca agc tct att gga aat tcc 240
123 Leu Phe Ser Ser Cys Met Pro Gln Gln Thr Ser Ser Ile Gly Asn Ser
124 65 70 75 80
126 atc att aac atg gac ccg ccg aag cat aca aaa atc cgt tca gtc gtg 288
127 Ile Ile Asn Met Asp Pro Pro Lys His Thr Lys Ile Arg Ser Val Val
128 85 90 95
130 aac aaa gcc ttt act ccg cgc gtg atg aag caa tgg gaa ccg aga att 336
131 Asn Lys Ala Phe Thr Pro Arg Val Met Lys Gln Trp Glu Pro Arg Ile
132 100 105 110
134 caa gaa atc aca gat gaa ctg att caa aaa ttt cag ggg cgc agt gag 384
135 Gln Glu Ile Thr Asp Glu Leu Ile Gln Lys Phe Gln Gly Arg Ser Glu
136 115 120 125
138 ttt gac ctt gtt cac gat ttt tca tac ccg ctt ccg gtt att gtg ata 432
139 Phe Asp Leu Val His Asp Phe Ser Tyr Pro Leu Pro Val Ile Val Ile

```

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Input Set : A:\PTO.AMC.txt

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140	130	135	140	
142	tct gag ctg ctg gga gtg cct tca gcg cat atg gaa cag ttt aaa gca	480		
143	Ser Glu Leu Leu Gly Val Pro Ser Ala His Met Glu Gln Phe Lys Ala			
144	145	150	155	160
146	tggtctgatcttctggtcagtagacacgcgaagatgaaagtgaagaaagt	528		
147	Trp Ser Asp Leu Leu Val Ser Thr Pro Lys Asp Lys Ser Glu Glu Ala			
148	165	170	175	
150	gaa aaa gcc ttt ttg gaa gaa cga gat aag tgt gag gaa gaa ctg gcc	576		
151	Glu Lys Ala Phe Leu Glu Glu Arg Asp Lys Cys Glu Glu Glu Leu Ala			
152	180	185	190	
154	gcgtttttgccggcattatagaa gaa aag cga aac aaa ccg gaa cag	624		
155	Ala Phe Phe Ala Gly Ile Ile Glu Glu Lys Arg Asn Lys Pro Glu Gln			
156	195	200	205	
158	gat att att tct att tta gtg gaa gcg gaa gaa aca ggc gag aag ctg	672		
159	Asp Ile Ile Ser Ile Leu Val Glu Ala Glu Glu Thr Gly Glu Lys Leu			
160	210	215	220	
162	tcc ggt gaa gag ctg att ccg ttt tgc acg ctg ctg ctg gtg gcc gga	720		
163	Ser Gly Glu Glu Leu Ile Pro Phe Cys Thr Leu Leu Leu Val Ala Gly			
164	225	230	235	240
166	aat gaa acc act aca aac ctg att tca aat gcg atg tac agc ata tta	768		
167	Asn Glu Thr Thr Thr Asn Leu Ile Ser Asn Ala Met Tyr Ser Ile Leu			
168	245	250	255	
170	gaa acg cca ggc gtt tac gag gaa ctg cgc agc cat cct gaa ctg atg	816		
171	Glu Thr Pro Gly Val Tyr Glu Glu Leu Arg Ser His Pro Glu Leu Met			
172	260	265	270	
174	cct cag gca gtg gag gaa gcc ttg cgt ttc aga gcg ccg gcc ccg gtt	864		
175	Pro Gln Ala Val Glu Glu Ala Leu Arg Phe Arg Ala Pro Ala Pro Val			
176	275	280	285	
178	ttg agg cgc att gcc aag cgg gat acg gag atc ggg ggg cac ctg att	912		
179	Leu Arg Arg Ile Ala Lys Arg Asp Thr Glu Ile Gly Gly His Leu Ile			
180	290	295	300	
182	aaa gaa ggt gat atg gtt ttg gcg ttt gtg gca tcg gca aat cgt gat	960		
183	Lys Glu Gly Asp Met Val Leu Ala Phe Val Ala Ser Ala Asn Arg Asp			
184	305	310	315	320
186	gaa gca aag ttt gac aga ccg cac atg ttt gat atc cgc cgc cat ccc	1008		
187	Glu Ala Lys Phe Asp Arg Pro His Met Phe Asp Ile Arg Arg His Pro			
188	325	330	335	
190	aat ccg cat att gcg ttt ggc cac ggc atc cat ttt tgc ctt ggg gcc	1056		
191	Asn Pro His Ile Ala Phe Gly His Gly Ile His Phe Cys Leu Gly Ala			
192	340	345	350	
194	ccg ctt gcc cgt ctt gaa gca aat atc gcg tta acg tct ttg att tct	1104		
195	Pro Leu Ala Arg Leu Glu Ala Asn Ile Ala Leu Thr Ser Leu Ile Ser			
196	355	360	365	
198	gct ttt cct cat atg gag tgc gtc agt atc act ccg att gaa aac agt	1152		
199	Ala Phe Pro His Met Glu Cys Val Ser Ile Thr Pro Ile Glu Asn Ser			
200	370	375	380	
202	gtg ata tac gga tta aag agc ttc cgt gtg aaa atg taa	1191		
203	Val Ile Tyr Gly Leu Lys Ser Phe Arg Val Lys Met			
204	385	390	395	

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Input Set : A:\PTO.AMC.txt

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207 <210> SEQ ID NO: 3
208 <211> LENGTH: 39
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Synthetic DNA
215 <400> SEQUENCE: 3
216 ttggtatccg aattcaaaag tgctggcgct gttccgttt 39
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 41
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Synthetic DNA
227 <400> SEQUENCE: 4
228 gtgggatccg tcgaccactt ttttcacgat gttcactccc c 41
231 <210> SEQ ID NO: 5
232 <211> LENGTH: 39
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Synthetic DNA
239 <400> SEQUENCE: 5
240 ccaggatcct ctagatggtg aaatggttgt tgccgctct 39
243 <210> SEQ ID NO: 6
244 <211> LENGTH: 39
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Synthetic DNA
251 <400> SEQUENCE: 6
252 tcaggatccc ccgggtgagc ggcaaatcca cccaccctg 39
255 <210> SEQ ID NO: 7
256 <211> LENGTH: 37
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Synthetic DNA
263 <400> SEQUENCE: 7
264 taagcgcgcc ccgggttaat tggatgggcy aaagctc 37
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 39
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Synthetic DNA
275 <400> SEQUENCE: 8
276 atcgcgcgcg tcgacgatag cggcagaaaa ttggcggca 39
279 <210> SEQ ID NO: 9

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Input Set : A:\PTO.AMC.txt

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```

280 <211> LENGTH: 38
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Synthetic DNA
287 <400> SEQUENCE: 9
288 agcggatccg aattcgctgg aatcaaaagt cggccaga      38
291 <210> SEQ ID NO: 10
292 <211> LENGTH: 38
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Synthetic DNA
299 <400> SEQUENCE: 10
300 tcaggatccg tcgactgaga aaacacaaac gccccctc      38
303 <210> SEQ ID NO: 11
304 <211> LENGTH: 39
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic DNA
311 <400> SEQUENCE: 11
312 atgggaccc ctacacatgt tgtagtttgg gttggaatc      39
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 42
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Synthetic DNA
323 <400> SEQUENCE: 12
324 gccggatcca gatctggcat cacacaacaa taaatacacc gc      42
327 <210> SEQ ID NO: 13
328 <211> LENGTH: 39
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Synthetic DNA
335 <400> SEQUENCE: 13
336 tctggatcct ctagaagaga acacaaagag tacgaatgc      39
339 <210> SEQ ID NO: 14
340 <211> LENGTH: 41
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Synthetic DNA
347 <400> SEQUENCE: 14
348 aaaggatccc ccgggtttac cagccagcgc aacaaagtca t      41
351 <210> SEQ ID NO: 15
352 <211> LENGTH: 39

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/869,334

DATE: 10/04/2001

TIME: 12:48:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:699 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:707 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:711 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:719 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:723 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:735 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:795 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:1001 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:1002 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44

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Input Set : A:\PTO.AMC.txt

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L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44